



ALIGNMENT 1: SEQ ID NO:7

Original Seq7	1	30	31	60	61	90	91	120
Substitute Seq7	GAATTCACGATGGCCAAACAAATACAATTCC		GAAATCCTGAACAATATCATCTGAACTCG		CGTTACAAAGACAACAATCTGATCGATCTG		TCTGGTTACGGTGTAAAGTTGAAGTATAC	
Amended Seq7	GAATTCACGATGGCCAAACAAATACAATTCC		GAAATCCTGAACAATATCATCTGAACTCG		CGTTACAAAGACAACAATCTGATCGATCTG		TCTGGTTACGGTGTAAAGTTGAAGTATAC	
Original Fig4	GAATTCACGATGGCCAAACAAATACAATTCC		GAAATCCTGAACAATATCATCTGAACTCG		CGTTACAAAGACAACAATCTGATCGATCTG		TCTGGTTACGGTGTAAAGTTGAAGTATAC	

Original Seq7	121	150	151	180	181	210	211	240
Substitute Seq7	GACGGTGTGAAGTGAATGACAAGAACCCAG		TTCAAAGTACCTCTTCCGCTAACTCTAAG		ATCCGTGTACTCAGAATCAGAACATCATC		TTCAACTCCGTATTCTCGGACTTCTCTGTT	
Amended Seq7	GACGGTGTGAAGTGAATGACAAGAACCCAG		TTCAAAGTACCTCTTCCGCTAACTCTAAG		ATCCGTGTACTCAGAATCAGAACATCATC		TTCAACTCCGTATTCTCGGACTTCTCTGTT	
Original Fig4	GACGGTGTGAAGTGAATGACAAGAACCCAG		TTCAAAGTACCTCTTCCGCTAACTCTAAG		ATCCGTGTACTCAGAATCAGAACATCATC		TTCAACTCCGTATTCTCGGACTTCTCTGTT	

Original Seq7	241	270	271	300	301	330	331	360
Substitute Seq7	TCCTTCTGGATTCGTATCCCGAAATACAAG		AACGACGGTATCCAGAATTACATCCACAAT		GAATACACCATCATCAACTGCATGAAGAAT		AACTCTGGTTGGAAGATCTCCATCCCGGT	
Amended Seq7	TCCTTCTGGATTCGTATCCCGAAATACAAG		AACGACGGTATCCAGAATTACATCCACAAT		GAATACACCATCATCAACTGCATGAAGAAT		AACTCTGGTTGGAAGATCTCCATCCCGGT	
Original Fig4	TCCTTCTGGATTCGTATCCCGAAATACAAG		AACGACGGTATCCAGAATTACATCCACAAT		GAATACACCATCATCAACTGCATGAAGAAT		AACTCTGGTTGGAAGATCTCCATCCCGGT	

Original Seq7	361	390	391	420	421	450	451	480
Substitute Seq7	AACCGTATCATCTGGACTCTGATCGATATC		AACGGTAAGACCAAACTGTATTCTTCGAA		TACAACATCCGTGAAGACATCTCTGAATAC		ATCAATCCGTGGTTCCTCGTTACCATCACC	
Amended Seq7	AACCGTATCATCTGGACTCTGATCGATATC		AACGGTAAGACCAAACTGTATTCTTCGAA		TACAACATCCGTGAAGACATCTCTGAATAC		ATCAATCCGTGGTTCCTCGTTACCATCACC	
Original Fig4	AACCGTATCATCTGGACTCTGATCGATATC		AACGGTAAGACCAAACTGTATTCTTCGAA		TACAACATCCGTGAAGACATCTCTGAATAC		ATCAATCCGTGGTTCCTCGTTACCATCACC	

Original Seq7	481	510	511	540	541	570	571	600
Substitute Seq7	AATAACCTGAACAATGCTAAAATCTACATC		AACGGTAACTGGAATCTAATACCGACATC		AAAGACATCCGTGAAGTTATCGCTAACGGT		GAAATCATCTTCAAAGTGGACGGTGACATC	
Amended Seq7	AATAACCTGAACAATGCTAAAATCTACATC		AACGGTAACTGGAATCTAATACCGACATC		AAAGACATCCGTGAAGTTATCGCTAACGGT		GAAATCATCTTCAAAGTGGACGGTGACATC	
Original Fig4	AATAACCTGAACAATGCTAAAATCTACATC		AACGGTAACTGGAATCTAATACCGACATC		AAAGACATCCGTGAAGTTATCGCTAACGGT		GAAATCATCTTCAAAGTGGACGGTGACATC	

Original Seq7	601	630	631	660	661	690	691	720
Substitute Seq7	GATCGTACCCAGTTTCATCTGGATGAAATAC		TTCTCCATCTTCAACACCGAAGTGTCTCAG		TCCAATATCGAAGAACCGTACAAGATCCAG		TCTTACTCCGAATACCTGAAAGACTTCTGG	
Amended Seq7	GATCGTACCCAGTTTCATCTGGATGAAATAC		TTCTCCATCTTCAACACCGAAGTGTCTCAG		TCCAATATCGAAGAACCGTACAAGATCCAG		TCTTACTCCGAATACCTGAAAGACTTCTGG	
Original Fig4	GATCGTACCCAGTTTCATCTGGATGAAATAC		TTCTCCATCTTCAACACCGAAGTGTCTCAG		TCCAATATCGAAGAACCGTACAAGATCCAG		TCTTACTCCGAATACCTGAAAGACTTCTGG	

Original Seq7	721	750	751	780	781	810	811	840
Substitute Seq7	GGTAATCCGCTGATGTACAACAAGAAATAC		TATATGTTCAATGCTGTTAACAAGAACTCT		TACATCAAAGTGAAGAAAGACTCTCCGGTT		GGTGAAATCCTGACTCGTTCCAAATACAAC	
Amended Seq7	GGTAATCCGCTGATGTACAACAAGAAATAC		TATATGTTCAATGCTGTTAACAAGAACTCT		TACATCAAAGTGAAGAAAGACTCTCCGGTT		GGTGAAATCCTGACTCGTTCCAAATACAAC	
Original Fig4	GGTAATCCGCTGATGTACAACAAGAAATAC		TATATGTTCAATGCTGTTAACAAGAACTCT		TACATCAAAGTGAAGAAAGACTCTCCGGTT		GGTGAAATCCTGACTCGTTCCAAATACAAC	

Original Seq7	841	870	871	900	901	930	931	960
Substitute Seq7	CAGAAGTCTAAATACATCAACTACCGCGAC		CTGTACATCGGTGAAAAGTTTCATCATCCGT		CGCAAACTCTAAGTCTCAGTCCATCAATGAT		GACATCGTACGTAAGAAAGACTACATCTAC	
Amended Seq7	CAGAAGTCTAAATACATCAACTACCGCGAC		CTGTACATCGGTGAAAAGTTTCATCATCCGT		CGCAAACTCTAAGTCTCAGTCCATCAATGAT		GACATCGTACGTAAGAAAGACTACATCTAC	
Original Fig4	CAGAAGTCTAAATACATCAACTACCGCGAC		CTGTACATCGGTGAAAAGTTTCATCATCCGT		CGCAAACTCTAAGTCTCAGTCCATCAATGAT		GACATCGTACGTAAGAAAGACTACATCTAC	

Original Seq7	961	990	991	1020	1021	1050	1051	1080
Substitute Seq7	CTGGACTTCTTCAACCTGAATCAGGAATGG		CGTGATACACCTACAAGTACTTCAAGAAA		GAAGAAGAAAAGCTTTTCTGGCTCCGATC		TCTGATTCCGACGAATCTACAACACCATC	
Amended Seq7	CTGGACTTCTTCAACCTGAATCAGGAATGG		CGTGATACACCTACAAGTACTTCAAGAAA		GAAGAAGAAAAGCTTTTCTGGCTCCGATC		TCTGATTCCGACGAATCTACAACACCATC	
Original Fig4	CTGGACTTCTTCAACCTGAATCAGGAATGG		CGTGATACACCTACAAGTACTTCAAGAAA		GAAGAAGAAAAGCTTTTCTGGCTCCGATC		TCTGATTCCGACGAATCTACAACACCATC	

Original Seq7	1081	1110	1111	1140	1141	1170	1171	1200
Substitute Seq7	CAGATCAAAGAATACGACGAACAGCCGACC		TACTCTTGCCAGCTGCTGTTCAAGAAAGAT		GAAGAATCTACTGACGAAATCGGTCTGATC		GGTATCCACCGTTTCTACGAATCTGGTATC	
Amended Seq7	CAGATCAAAGAATACGACGAACAGCCGACC		TACTCTTGCCAGCTGCTGTTCAAGAAAGAT		GAAGAATCTACTGACGAAATCGGTCTGATC		GGTATCCACCGTTTCTACGAATCTGGTATC	
Original Fig4	CAGATCAAAGAATACGACGAACAGCCGACC		TACTCTTGCCAGCTGCTGTTCAAGAAAGAT		GAAGAATCTACTGACGAAATCGGTCTGATC		GGTATCCACCGTTTCTACGAATCTGGTATC	

Original Seq7	1201	1230	1231	1260	1261	1290	1291	1320
Substitute Seq7	GTATTGGAAGATACAAAGACTACTTCTGC		ATCTCCAAATGGTACCTGAAGGAAGTTAAA		CGCAAAACCGTACAACCTGAACTGGGTGTC		AATTGGCAGTTTCATCCGAAAGACGAAGGT	
Amended Seq7	GTATTGGAAGATACAAAGACTACTTCTGC		ATCTCCAAATGGTACCTGAAGGAAGTTAAA		CGCAAAACCGTACAACCTGAACTGGGTGTC		AATTGGCAGTTTCATCCGAAAGACGAAGGT	
Original Fig4	GTATTGGAAGATACAAAGACTACTTCTGC		ATCTCCAAATGGTACCTGAAGGAAGTTAAA		CGCAAAACCGTACAACCTGAACTGGGTGTC		AATTGGCAGTTTCATCCGAAAGACGAAGGT	

Original Seq7	1321	1341						
Substitute Seq7	TGGACCGAATAGTAAGAATTC							
Amended Seq7	TGGACCGAATAGTAAGAATTC							
Original Fig4	TGGACCGAATAGTAAGAATTC							

ALIGNMENT 2: SEQ ID NO:37

Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1 CTCGAGCCATGGCTCGTCTGCTGTCTAAGT CTCGAGCCATGGCTCGTCTGCTGTCTAAGT CTCGAGCCATGGCTCGTCTGCTGTCTAAGT CTCGAGCCATGGCTCGTCTGCTGTCTAAGT *****	30 TCAGTGAATACATCAAGAATCATCAATA TCAGTGAATACATCAAGAATCATCAATA TCAGTGAATACATCAAGAATCATCAATA TCAGTGAATACATCAAGAATCATCAATA *****	60 CCTCCATCTGAACTGCGCTACGAATCCA CCTCCATCTGAACTGCGCTACGAATCCA CCTCCATCTGAACTGCGCTACGAATCCA CCTCCATCTGAACTGCGCTACGAATCCA *****	90 ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT ATCACCTGATCGACCTGTCTCGCTACGCTT *****	120
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	121 CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT CCAAAATCAACATCGGTTCTAAAGTTAACT *****	150 TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATCGACAAGAATCAGATCCAGC *****	180 TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG *****	210 TTATCTCTGAAGAAATGCTATCGTATACAAT TTATCTCTGAAGAAATGCTATCGTATACAAT TTATCTCTGAAGAAATGCTATCGTATACAAT TTATCTCTGAAGAAATGCTATCGTATACAAT *****	240
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	241 CTATGTACGAAAACCTTCTCCACCTCTCTCT CTATGTACGAAAACCTTCTCCACCTCTCTCT CTATGTACGAAAACCTTCTCCACCTCTCTCT CTATGTACGAAAACCTTCTCCACCTCTCTCT *****	270 GGATCCGATCTCCGAAATCTTCAACTCCA GGATCCGATCTCCGAAATCTTCAACTCCA GGATCCGATCTCCGAAATCTTCAACTCCA GGATCCGATCTCCGAAATCTTCAACTCCA *****	300 TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA *****	330 ACTGATGAAAAACAAATCTTGGTTGGAAAG ACTGATGAAAAACAAATCTTGGTTGGAAAG ACTGATGAAAAACAAATCTTGGTTGGAAAG ACTGATGAAAAACAAATCTTGGTTGGAAAG *****	360
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	361 TATCTCTGAACACCGTGAAATCATCTGGA TATCTCTGAACACCGTGAAATCATCTGGA TATCTCTGAACACCGTGAAATCATCTGGA TATCTCTGAACACCGTGAAATCATCTGGA *****	390 CTCTGCAGGACACTCAGGAATCAACACAGC CTCTGCAGGACACTCAGGAATCAACACAGC CTCTGCAGGACACTCAGGAATCAACACAGC CTCTGCAGGACACTCAGGAATCAACACAGC *****	420 GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA *****	450 ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT *****	480
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	481 TCGTTACCACACCAACATCGTCTGAATA TCGTTACCACACCAACATCGTCTGAATA TCGTTACCACACCAACATCGTCTGAATA TCGTTACCACACCAACATCGTCTGAATA *****	510 ACTCCAAAATCTACATCAACGTCGCTCTGA ACTCCAAAATCTACATCAACGTCGCTCTGA ACTCCAAAATCTACATCAACGTCGCTCTGA ACTCCAAAATCTACATCAACGTCGCTCTGA *****	540 TCGACAGAAACCGATCTCCAATCTGGGTA TCGACAGAAACCGATCTCCAATCTGGGTA TCGACAGAAACCGATCTCCAATCTGGGTA TCGACAGAAACCGATCTCCAATCTGGGTA *****	570 ACATCCACGTTCTTAATAACATCATGTTCA ACATCCACGTTCTTAATAACATCATGTTCA ACATCCACGTTCTTAATAACATCATGTTCA ACATCCACGTTCTTAATAACATCATGTTCA *****	600
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	601 AATCGGACGGTTGCTGACACTCACCCTG AATCGGACGGTTGCTGACACTCACCCTG AATCGGACGGTTGCTGACACTCACCCTG AATCGGACGGTTGCTGACACTCACCCTG *****	630 ACATCTGGATCAAAATCTTCAATCTGTTTC ACATCTGGATCAAAATCTTCAATCTGTTTC ACATCTGGATCAAAATCTTCAATCTGTTTC ACATCTGGATCAAAATCTTCAATCTGTTTC *****	660 ACAAAGAACTGAACGAAAAAGAAATCAAG ACAAAGAACTGAACGAAAAAGAAATCAAG ACAAAGAACTGAACGAAAAAGAAATCAAG ACAAAGAACTGAACGAAAAAGAAATCAAG *****	690 ACCTGTACGACACCAAGTCCAATCTCGGTA ACCTGTACGACACCAAGTCCAATCTCGGTA ACCTGTACGACACCAAGTCCAATCTCGGTA ACCTGTACGACACCAAGTCCAATCTCGGTA *****	720
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	721 TCCGTGAAAGACTTCTGGGGTGACTACCTGC TCCGTGAAAGACTTCTGGGGTGACTACCTGC TCCGTGAAAGACTTCTGGGGTGACTACCTGC TCCGTGAAAGACTTCTGGGGTGACTACCTGC *****	750 AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC *****	780 TGTCACGATCCGAAACAAATACGTTGACGTC TGTCACGATCCGAAACAAATACGTTGACGTC TGTCACGATCCGAAACAAATACGTTGACGTC TGTCACGATCCGAAACAAATACGTTGACGTC *****	810 ACAATGTAGGTATCCCGGGTTACATGTACC ACAATGTAGGTATCCCGGGTTACATGTACC ACAATGTAGGTATCCCGGGTTACATGTACC ACAATGTAGGTATCCCGGGTTACATGTACC *****	840
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	841 TGAAGGTCGCGCTGGTTCTGTTATGACTA TGAAGGTCGCGCTGGTTCTGTTATGACTA TGAAGGTCGCGCTGGTTCTGTTATGACTA TGAAGGTCGCGCTGGTTCTGTTATGACTA *****	870 CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC CCAACATCTACCTGAACTCTTCCCTGTACC *****	900 GTGGTACCAAAATTCATCATCAAGAAATACG GTGGTACCAAAATTCATCATCAAGAAATACG GTGGTACCAAAATTCATCATCAAGAAATACG GTGGTACCAAAATTCATCATCAAGAAATACG *****	930 CGTCTGGTAAACAGGACAATATGTTTCGCA CGTCTGGTAAACAGGACAATATGTTTCGCA CGTCTGGTAAACAGGACAATATGTTTCGCA CGTCTGGTAAACAGGACAATATGTTTCGCA *****	960
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	961 ACAATGATCGGTATACATCAATGTTGTAG ACAATGATCGGTATACATCAATGTTGTAG ACAATGATCGGTATACATCAATGTTGTAG ACAATGATCGGTATACATCAATGTTGTAG *****	990 TTAAGAACAAAGAAATACCGTCTGGCTACCA TTAAGAACAAAGAAATACCGTCTGGCTACCA TTAAGAACAAAGAAATACCGTCTGGCTACCA TTAAGAACAAAGAAATACCGTCTGGCTACCA *****	1020 ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT *****	1050 TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA *****	1080
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1081 ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA *****	1110 AGAACGACCAAGGATCTACTAACAATGCA AGAACGACCAAGGATCTACTAACAATGCA AGAACGACCAAGGATCTACTAACAATGCA AGAACGACCAAGGATCTACTAACAATGCA *****	1140 AAATGAATCTGCAGGACAACAAATGGAACG AAATGAATCTGCAGGACAACAAATGGAACG AAATGAATCTGCAGGACAACAAATGGAACG AAATGAATCTGCAGGACAACAAATGGAACG *****	1170 ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA *****	1200
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1201 ACAATATCGCTAACTGGTTGCTTCCAAC ACAATATCGCTAACTGGTTGCTTCCAAC ACAATATCGCTAACTGGTTGCTTCCAAC ACAATATCGCTAACTGGTTGCTTCCAAC *****	1230 GGTACAATCGTCAGATCGAACGTTCTCTCTC GGTACAATCGTCAGATCGAACGTTCTCTCTC GGTACAATCGTCAGATCGAACGTTCTCTCTC GGTACAATCGTCAGATCGAACGTTCTCTCTC *****	1260 GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC *****	1290 CGGTTGATGACCGTTGGGGTGAAAGCTCCGC CGGTTGATGACCGTTGGGGTGAAAGCTCCGC CGGTTGATGACCGTTGGGGTGAAAGCTCCGC CGGTTGATGACCGTTGGGGTGAAAGCTCCGC *****	1320
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1321 TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT *****	1338 TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT *****			

ALIGNMENT 3: SEQ ID NO:39

Original_Seq39	1	30	31	60	61	90	91	120
Substitute_Seq39	ATGGC	CAACAAATACAATTCGAAATC	CTGAACAATATCATCTGAACTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGTCAAAGTTGAAGTATACGACGGT			
Amended_Seq39	ATGGC	CAACAAATACAATTCGAAATC	CTGAACAATATCATCTGAACTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGTCAAAGTTGAAGTATACGACGGT			
Fig4_ '975_App	ATGGC	CAACAAATACAATTCGAAATC	CTGAACAATATCATCTGAACTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGTCAAAGTTGAAGTATACGACGGT			
	*****	*****	*****	*****	*****			
	121	150	151	180	181	210	211	240
Original_Seq39	GTTGAACTGAATGACAAGAACAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
Substitute_Seq39	GTTGAACTGAATGACAAGAACAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
Amended_Seq39	GTTGAACTGAATGACAAGAACAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
Fig4_ '975_App	GTTGAACTGAATGACAAGAACAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
	*****	*****	*****	*****				
	241	270	271	300	301	330	331	360
Original_Seq39	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
Substitute_Seq39	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
Amended_Seq39	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
Fig4_ '975_App	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
	*****	*****	*****	*****				
	361	390	391	420	421	450	451	480
Original_Seq39	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTCTCGTTACCACCAATAAAC				
Substitute_Seq39	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTCTCGTTACCACCAATAAAC				
Amended_Seq39	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTCTCGTTACCACCAATAAAC				
Fig4_ '975_App	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTCTCGTTACCACCAATAAAC				
	*****	*****	*****	*****				
	481	510	511	540	541	570	571	600
Original_Seq39	CTGAACAATGCTAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
Substitute_Seq39	CTGAACAATGCTAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
Amended_Seq39	CTGAACAATGCTAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
Fig4_ '975_App	CTGAACAATGCTAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
	*****	*****	*****	*****				
	601	630	631	660	661	690	691	720
Original_Seq39	ACCCAGTTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAACTGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
Substitute_Seq39	ACCCAGTTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAACTGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
Amended_Seq39	ACCCAGTTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAACTGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
Fig4_ '975_App	ACCCAGTTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAACTGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
	*****	*****	*****	*****				
	721	750	751	780	781	810	811	840
Original_Seq39	CCGCTGATGTACAACAAGAAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTGACTCGTTTCAAATACAACAGAAC				
Substitute_Seq39	CCGCTGATGTACAACAAGAAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTGACTCGTTTCAAATACAACAGAAC				
Amended_Seq39	CCGCTGATGTACAACAAGAAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTGACTCGTTTCAAATACAACAGAAC				
Fig4_ '975_App	CCGCTGATGTACAACAAGAAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTGACTCGTTTCAAATACAACAGAAC				
	*****	*****	*****	*****				
	841	870	871	900	901	930	931	960
Original_Seq39	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGATGACATC	GTACGTAAAGAAAGACTACATCTACCTGGAC				
Substitute_Seq39	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGATGACATC	GTACGTAAAGAAAGACTACATCTACCTGGAC				
Amended_Seq39	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGATGACATC	GTACGTAAAGAAAGACTACATCTACCTGGAC				
Fig4_ '975_App	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGATGACATC	GTACGTAAAGAAAGACTACATCTACCTGGAC				
	*****	*****	*****	*****				
	961	990	991	1020	1021	1050	1051	1080
Original_Seq39	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAAAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACTCTACAACCATCCAGATC				
Substitute_Seq39	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAAAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACTCTACAACCATCCAGATC				
Amended_Seq39	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAAAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACTCTACAACCATCCAGATC				
Fig4_ '975_App	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAAAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACTCTACAACCATCCAGATC				
	*****	*****	*****	*****				
	1081	1110	1111	1140	1141	1170	1171	1200
Original_Seq39	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
Substitute_Seq39	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
Amended_Seq39	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
Fig4_ '975_App	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
	*****	*****	*****	*****				
	1201	1230	1231	1260	1261	1290	1291	1320
Original_Seq39	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTTCATCCCGAAAGACGAAGTTGGACC				
Substitute_Seq39	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTTCATCCCGAAAGACGAAGTTGGACC				
Amended_Seq39	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTTCATCCCGAAAGACGAAGTTGGACC				
Fig4_ '975_App	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTTCATCCCGAAAGACGAAGTTGGACC				
	*****	*****	*****	*****				
	1321	1350	1351					
Original_Seq39	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						
Substitute_Seq39	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						
Amended_Seq39	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						
Fig4_ '975_App	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						
	*****	*****						

ALIGNMENT 4: SEQ ID NO:40

Original_Seq40	1	30 31	60 61	90 91	120
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	MPVTINNFNYPNDPIDNNNIIMMEPPFARGT	GRYYKAFKITDRIWIIIPERYTPGYKPEDFN	KSSGIFNRDVCYYDDPYLNTNDKKNIFLO	TMIKLFNRKIKSKPLGKLEMIINGIPYLG	
Original_Seq40	121	150 151	180 181	210 211	240
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	DRRVPLEEFNTNIASVTNKLISNPGEVER	KKGIFANLIIFGPGPVLNENETIDIGIQNH	PASREGFGGIMQMKFCPEYVSFVNNVQENK	GASIFNRRGYFSDPALILMHLEIHLVHLGLY	
Original_Seq40	241	270 271	300 301	330 331	360
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	GIKVDDLPIVNEKKFFMQSTDAIQAEELY	TFGGQDPSIITPSTDKSIYDKVLQNFGRIV	DRLNKVLVCISDPNININIIYKNKFKDKYKF	VEDSEGKYSIDVESFDKLYKSLMFGFTETN	
Original_Seq40	361	390 391	420 421	450 451	480
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	IAENYKIKTRASYSFSDSLPPVKIKNLLDNE	IYTIIEGFNISDKMEKEYRGQNKAIKQQA	YEEISKEHLAVYKIQMCKSVKAPGICIDVD	NEDLFFIADKNSFSDLSKNERIEYNTQSN	
Original_Seq40	481	510 511	540 541	570 571	600
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	YIENDFPINELILDTLISKIELPSENTES	LTDNFVDVPVYEKQPAIKKIPTDENTIFQY	LYSQTPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLPAGWVQIVND	
Original_Seq40	601	630 631	660 661	690 691	720
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	FVIEANKSNTMDKDIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTQRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	
Original_Seq40	721	750 751	780 781	810 811	840
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	KALNYQAQALEEIIKYRYNIYSEKEKSNIN	IDFNDINSKLNIGINQAIDNINNFIGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI	DENKLYLIGSAEYKSVKNYKLTIMPFDL	
Original_Seq40	841	870 871	900 901	930 931	960
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	-----FNKYNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	-----FNKYNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	-----FNKYNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	SIYTNDTILIEMFNKNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	*****	*****	*****	*****	
Original_Seq40	961	990 991	1020 1021	1050 1051	1080
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	GWKISIRGNRIWTLIDINGKTKSVFFEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIPNTELSQSNIEERYKIQSY	
	GWKISIRGNRIWTLIDINGKTKSVFFEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIPNTELSQSNIEERYKIQSY	
	GWKISIRGNRIWTLIDINGKTKSVFFEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIPNTELSQSNIEERYKIQSY	
	*****	*****	*****	*****	
Original_Seq40	1081	1110 1111	1140 1141	1170 1171	1200
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	SEYLDKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVRVYTYKFKKEEKLFLAPISD	
	SEYLDKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVRVYTYKFKKEEKLFLAPISD	
	SEYLDKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVRVYTYKFKKEEKLFLAPISD	
	*****	*****	*****	*****	
Original_Seq40	1201	1230 1231	1260 1261	1290 1291	
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKKRPYNLKLGCNWQFIPKDEGWT	E	
	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKKRPYNLKLGCNWQFIPKDEGWT	E	
	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKKRPYNLKLGCNWQFIPKDEGWT	E	
	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKKRPYNLKLGCNWQFIPKDEGWT	E	
	*****	*****	*****	*****	

ALIGNMENT 5: SEQ ID NO:41

Original_Seq41	1	30 31	60 61	90 91	120
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	MQFVNKQPNFYKDPVNGVDIAYIKIPNVGQM	QPVKAFKIHKNWIVPERDFTFNPEEGDLN	PPPEAKQVPVSYDYDSTYLSTDNKDNLYLKG	VTKLPERIYSTDLGRMLLTSIVRGIPFWGG	
Original_Seq41	121	150 151	180 181	210 211	240
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	STIDTELKVIDTNCINVIQPDGYSRSEELN	LVIIGPSADI IQFECKSPGHEVLNLTRNGY	GSTQYIRFSPDFTFGPEESLEVDTNPLLGA	GKPADTDPAVTLAHELHAGHRLYGIAINPN	
Original_Seq41	241	270 271	300 301	330 331	360
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	RVFKVNTNAYEYMSGLEVSFEELRTFGGHD	AKFIDSLQENEPRLYYNFKDIASTLNKA	KSIVGTTASLQYMKNVPEKYLLEDSTSGK	FSDVKLKFDPKLYKMLTEIYTEDNFVKPFKV	
Original_Seq41	361	390 391	420 421	450 451	480
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	LNRKTYLNFDAVKFINIVPKVNYTIYDGF	NLRNTLNAAFNFGQNTENNMMFTKLKNFT	GLFEFYKLLCVRGIIITSKTKSLDKYGNKAL	NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE	NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
				NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE	NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
				*****	*****
Original_Seq41	481	510 511	540 541	570 571	600
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	ITSNTNIEAAEENISLDLIQQYYLTFNFDN	EPENISIEENLSSDIIGQLELMPNIERPNG	KKYELDKYTMFHYLRAQEFHKGSRIALTN	SVNEALLNPSRVYTFSSDYVKKVNKATEA	SVNEALLNPSRVYTFSSDYVKKVNKATEA
	ITSNTNIEAAEENISLDLIQQYYLTFNFDN	EPENISIEENLSSDIIGQLELMPNIERPNG	KKYELDKYTMFHYLRAQEFHKGSRIALTN	SVNEALLNPSRVYTFSSDYVKKVNKATEA	SVNEALLNPSRVYTFSSDYVKKVNKATEA
	*****	*****	*****	*****	*****
Original_Seq41	601	630 631	660 661	690 691	720
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIPYIGPALNIGMLYKDDFVGALIFSG	AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTIIDNALSKRNEKWDEVYKIVTNWLAK	TVQTIIDNALSKRNEKWDEVYKIVTNWLAK
	AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIPYIGPALNIGMLYKDDFVGALIFSG	AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTIIDNALSKRNEKWDEVYKIVTNWLAK	TVQTIIDNALSKRNEKWDEVYKIVTNWLAK
	AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIPYIGPALNIGMLYKDDFVGALIFSG	AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTIIDNALSKRNEKWDEVYKIVTNWLAK	TVQTIIDNALSKRNEKWDEVYKIVTNWLAK
	*****	*****	*****	*****	*****
Original_Seq41	721	750 751	780 781	810 811	840
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	VNTQIDILIRKKMKEALENQAATKAIINYO	YNQYTEEEKNNINFNIDDLSSKLNESINKA	MININKFLNQCSVSYLMNSMIPYGVKRLD	FDASLKDALKYIDNNGTGLIGQVDRKDK	FDASLKDALKYIDNNGTGLIGQVDRKDK
	VNTQIDILIRKKMKEALENQAATKAIINYO	YNQYTEEEKNNINFNIDDLSSKLNESINKA	MININKFLNQCSVSYLMNSMIPYGVKRLD	FDASLKDALKYIDNNGTGLIGQVDRKDK	FDASLKDALKYIDNNGTGLIGQVDRKDK
	VNTQIDILIRKKMKEALENQAATKAIINYO	YNQYTEEEKNNINFNIDDLSSKLNESINKA	MININKFLNQCSVSYLMNSMIPYGVKRLD	FDASLKDALKYIDNNGTGLIGQVDRKDK	FDASLKDALKYIDNNGTGLIGQVDRKDK
	*****	*****	*****	*****	*****
Original_Seq41	841	870 871	900 901	930 931	960
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	VNNTLSTDIPFQLSKYVDNQRLNSTFTTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI	GSKVNFDPIDKNQIQLFNLESSKIEVILKN	AIVVNSMYENFSTFSWIRIPKYFNSISLNN	AIVVNSMYENFSTFSWIRIPKYFNSISLNN
	VNNTLSTDIPFQLSKYVDNQRLNSTFTTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI	GSKVNFDPIDKNQIQLFNLESSKIEVILKN	AIVVNSMYENFSTFSWIRIPKYFNSISLNN	AIVVNSMYENFSTFSWIRIPKYFNSISLNN
	VNNTLSTDIPFQLSKYVDNQRLNSTFTTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI	GSKVNFDPIDKNQIQLFNLESSKIEVILKN	AIVVNSMYENFSTFSWIRIPKYFNSISLNN	AIVVNSMYENFSTFSWIRIPKYFNSISLNN
	*****	*****	*****	*****	*****
Original_Seq41	961	990 991	1020 1021	1050 1051	1080
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	EYTIINCMMENNSGWKVSINYEIINTLQDT	QEIQRVVFYKYSQMINISDYINRWIFVTIT	NNRLNNSKIYINGRLIDQKPISNLGNLHA	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL
	EYTIINCMMENNSGWKVSINYEIINTLQDT	QEIQRVVFYKYSQMINISDYINRWIFVTIT	NNRLNNSKIYINGRLIDQKPISNLGNLHA	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL
	EYTIINCMMENNSGWKVSINYEIINTLQDT	QEIQRVVFYKYSQMINISDYINRWIFVTIT	NNRLNNSKIYINGRLIDQKPISNLGNLHA	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL
	*****	*****	*****	*****	*****
Original_Seq41	1081	1110 1111	1140 1141	1170 1171	1200
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	NEKEIKDLYDNQNSGILKDFWGDYLYQYDK	PYYMILLYDPNKYVDVNNVGIRGYMYLKG	RGSVMTTNIYLNSSLYRGTKPIIKKASGN	KDNIVRNNDRVYINVVVKNKEYRLATNASQ	KDNIVRNNDRVYINVVVKNKEYRLATNASQ
	NEKEIKDLYDNQNSGILKDFWGDYLYQYDK	PYYMILLYDPNKYVDVNNVGIRGYMYLKG	RGSVMTTNIYLNSSLYRGTKPIIKKASGN	KDNIVRNNDRVYINVVVKNKEYRLATNASQ	KDNIVRNNDRVYINVVVKNKEYRLATNASQ
	NEKEIKDLYDNQNSGILKDFWGDYLYQYDK	PYYMILLYDPNKYVDVNNVGIRGYMYLKG	RGSVMTTNIYLNSSLYRGTKPIIKKASGN	KDNIVRNNDRVYINVVVKNKEYRLATNASQ	KDNIVRNNDRVYINVVVKNKEYRLATNASQ
	*****	*****	*****	*****	*****
Original_Seq41	1201	1230 1231	1260 1261	1290 1297	
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	AGVEKILSALEIPDVGNLSQVVMKSKNDQ	GITNCKMNLQDNNGNDIGFIGFHQFNIA	KLVASNWNRYNTERSSRTLGCSEWIFPVDD	GWGERPL	GWGERPL
	AGVEKILSALEIPDVGNLSQVVMKSKNDQ	GITNCKMNLQDNNGNDIGFIGFHQFNIA	KLVASNWNRYNTERSSRTLGCSEWIFPVDD	GWGERPL	GWGERPL
	AGVEKILSALEIPDVGNLSQVVMKSKNDQ	GITNCKMNLQDNNGNDIGFIGFHQFNIA	KLVASNWNRYNTERSSRTLGCSEWIFPVDD	GWGERPL	GWGERPL
	*****	*****	*****	*****	*****

ALIGNMENT 6: SEQ ID NO:42

Original_Seq42	1	30 31	60 61	90 91	120
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	MPVTINNPNYNDPIDNNNIIMMEPPFARGT	GRYYKAFKITDRIWIIPERYTFGYKPEDFN	KSSGIFNRDVCEYYDPDYLTNDKKNIFLQ	TMIKLFNRIKSKPLGKLEMIINGIPYLG	
Original_Seq42	121	150 151	180 181	210 211	240
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	DRRVPLEEFNTNIASVTVNKLISNPGEVER	KKGIFANLIIFGPGVPLENENETIDIGIQNH	PASREGFGGIMQMKFCPEYVSFVNNVQENK	GASIFNRRGYFSDPALILMHLEIHLVHLGLY	
Original_Seq42	241	270 271	300 301	330 331	360
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	GIKVDDLPIVPNEKFFMQSDAIQAEELY	TFGGQDPSIITPSTDKSIYDKVLQNFGRIV	DRLNKVLVCISDPNININIKNFKDKYKF	VEDSEGKYSIDVESFDKLYKSLMFGFTETN	
Original_Seq42	361	390 391	420 421	450 451	480
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	IAENYKIKTRASYFSDSLPVKIKNLLDNE	IYTIIEGFNISDKDMEKEYRGQNKAINKQA	YEEISKEHLAVYKIQMCKSVKAPGICIDV	-----APGICIDVD	NEDLFFIADKNSFSDLSKNERIEYNTQSN
				-----APGICIDVD	NEDLFFIADKNSFSDLSKNERIEYNTQSN
				-----APGICIDVD	NEDLFFIADKNSFSDLSKNERIEYNTQSN
				*****	*****
Original_Seq42	481	510 511	540 541	570 571	600
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	YIENDFPINELILDITDLISKIELPSENTES	LTDFNVDPVYVEKQPAIKKIPTDENTIFQY	LYSQTFFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGVWKQIVND	
	YIENDFPINELILDITDLISKIELPSENTES	LTDFNVDPVYVEKQPAIKKIPTDENTIFQY	LYSQTFFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGVWKQIVND	
	YIENDFPINELILDITDLISKIELPSENTES	LTDFNVDPVYVEKQPAIKKIPTDENTIFQY	LYSQTFFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGVWKQIVND	
	*****	*****	*****	*****	*****
Original_Seq42	601	630 631	660 661	690 691	720
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTTRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	
	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTTRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	
	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTTRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	
	*****	*****	*****	*****	*****
Original_Seq42	721	750 751	780 781	810 811	840
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	KALNYQAQALEEIIKYRYNIYSEKEKSIN	IDFNDINSKLNEGINQAIDNINNPFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLNLYI	DENKLYLIGSAEYKSKVNKYLKTI MPFDL	
	KALNYQAQALEEIIKYRYNIYSEKEKSIN	IDFNDINSKLNEGINQAIDNINNPFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLNLYI	DENKLYLIGSAEYKSKVNKYLKTI MPFDL	
	KALNYQAQALEEIIKYRYNIYSEKEKSIN	IDFNDINSKLNEGINQAIDNINNPFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLNLYI	DENKLYLIGSAEYKSKVNKYLKTI MPFDL	
	*****	*****	*****	*****	*****
Original_Seq42	841	870 871	900 901	930 931	960
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	SIYTNDTILIEFMFNKYNSEILNIIILNRY	KDNNLIDLSGYAKVEYDGVDELNDKNQPK	LTSSANSKIRITQNONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS	
	SIYTNDTILIEFMFNKYNSEILNIIILNRY	KDNNLIDLSGYAKVEYDGVDELNDKNQPK	LTSSANSKIRITQNONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS	
	SIYTNDTILIEFMFNKYNSEILNIIILNRY	KDNNLIDLSGYAKVEYDGVDELNDKNQPK	LTSSANSKIRITQNONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS	
	*****	*****	*****	*****	*****
Original_Seq42	961	990 991	1020 1021	1050 1051	1080
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	GWKISIRGNRIIWTLIDINGKTKSVFFEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDI DR	TQFIWMKYFSIFNTELSQSNIERYKIQSY	
	GWKISIRGNRIIWTLIDINGKTKSVFFEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDI DR	TQFIWMKYFSIFNTELSQSNIERYKIQSY	
	GWKISIRGNRIIWTLIDINGKTKSVFFEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDI DR	TQFIWMKYFSIFNTELSQSNIERYKIQSY	
	*****	*****	*****	*****	*****
Original_Seq42	1081	1110 1111	1140 1141	1170 1171	1200
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKDSPVGEILTRSKYNQNSKYINRYDL	YIGKEPFIIRKKSNSQSINDDIVRKEDYIYL	DFPNLNQEWVRVYTYKPKKEEELFLAPIS	
	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKDSPVGEILTRSKYNQNSKYINRYDL	YIGKEPFIIRKKSNSQSINDDIVRKEDYIYL	DFPNLNQEWVRVYTYKPKKEEELFLAPIS	
	SEYLKDFWGNPLMYNKEYYMFNAGNKNSY	IKLKKDSPVGEILTRSKYNQNSKYINRYDL	YIGKEPFIIRKKSNSQSINDDIVRKEDYIYL	DFPNLNQEWVRVYTYKPKKEEELFLAPIS	
	*****	*****	*****	*****	*****
Original_Seq42	1201	1230 1231	1260 1261	1290 1292	
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE	ESTDEIGLIGIHRFYESGIVFEEKDFCI	SKWYLEVKKRPYNLKLGCNWQPIPKDEGW	TE	
	DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE	ESTDEIGLIGIHRFYESGIVFEEKDFCI	SKWYLEVKKRPYNLKLGCNWQPIPKDEGW	TE	
	DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE	ESTDEIGLIGIHRFYESGIVFEEKDFCI	SKWYLEVKKRPYNLKLGCNWQPIPKDEGW	TE	
	*****	*****	*****	*****	*****